

SEQUENCE LISTING

<110> Albone, Earl F.
Soltis, Daniel A.

<120> ANTIBODIES THAT BIND CELL-ASSOCIATED
CA 125/0772P AND METHODS OF USE THEREOF

<130> 6750-214-999

<140> To be assigned
<141> 2003-10-15

<150> 60/485,986
<151> 2003-07-10

<150> 60/418,828
<151> 2003-10-12

<160> 71

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 748
<212> PRT
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<400> 1
Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr Lys Leu Phe Thr His
1 5 10 15
Arg Ser Ser Val Ser Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr
20 25 30
Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala
35 40 45
Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
50 55 60
Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr
65 70 75 80
Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
85 90 95
Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
100 105 110
Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro
115 120 125
Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu
130 135 140
Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
145 150 155 160
Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
165 170 175
Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe
180 185 190
Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser
195 200 205
Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro

210	215	220													
Leu	Phe	Gln	Arg	Ser	Ser	Leu	Gly	Ala	Arg	Tyr	Thr	Gly	Cys	Arg	Val
225						230				235					240
Ile	Ala	Leu	Arg	Ser	Val	Lys	Asn	Gly	Ala	Glu	Thr	Arg	Val	Asp	Leu
						245				250					255
Leu	Cys	Thr	Tyr	Leu	Gln	Pro	Leu	Ser	Gly	Pro	Gly	Leu	Pro	Ile	Lys
						260			265						270
Gln	Val	Phe	His	Glu	Leu	Ser	Gln	Gln	Thr	His	Gly	Ile	Thr	Arg	Leu
						275			280						285
Gly	Pro	Tyr	Ser	Leu	Asp	Lys	Asp	Ser	Leu	Tyr	Leu	Asn	Gly	Tyr	Asn
						290			295						300
Glu	Pro	Gly	Pro	Asp	Glu	Pro	Pro	Thr	Thr	Pro	Lys	Pro	Ala	Thr	Thr
						305			310			315			320
Phe	Leu	Pro	Pro	Leu	Ser	Glu	Ala	Thr	Thr	Ala	Met	Gly	Tyr	His	Leu
						325			330						335
Lys	Thr	Leu	Thr	Leu	Asn	Phe	Thr	Ile	Ser	Asn	Leu	Gln	Tyr	Ser	Pro
						340			345						350
Asp	Met	Gly	Lys	Gly	Ser	Ala	Thr	Phe	Asn	Ser	Thr	Glu	Gly	Val	Leu
						355			360						365
Gln	His	Leu	Leu	Arg	Pro	Leu	Phe	Gln	Lys	Ser	Ser	Met	Gly	Pro	Phe
						370			375						380
Tyr	Leu	Gly	Cys	Gln	Leu	Ile	Ser	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Ala
						385			390			395			400
Ala	Thr	Gly	Val	Asp	Thr	Thr	Cys	Thr	Tyr	His	Pro	Asp	Pro	Val	Gly
						405			410						415
Pro	Gly	Leu	Asp	Ile	Gln	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr
						420			425						430
His	Gly	Val	Thr	Gln	Leu	Gly	Phe	Tyr	Val	Leu	Asp	Arg	Asp	Ser	Leu
						435			440			445			
Phe	Ile	Asn	Gly	Tyr	Ala	Pro	Gln	Asn	Leu	Ser	Ile	Arg	Gly	Glu	Tyr
						450			455			460			
Gln	Ile	Asn	Phe	His	Ile	Val	Asn	Trp	Asn	Leu	Ser	Asn	Pro	Asp	Pro
						465			470			475			480
Thr	Ser	Ser	Glu	Tyr	Ile	Thr	Leu	Leu	Arg	Asp	Ile	Gln	Asp	Lys	Val
						485			490			495			
Thr	Thr	Leu	Tyr	Lys	Gly	Ser	Gln	Leu	His	Asp	Thr	Phe	Arg	Phe	Cys
						500			505			510			
Leu	Val	Thr	Asn	Leu	Thr	Met	Asp	Ser	Val	Leu	Val	Thr	Val	Lys	Ala
						515			520			525			
Leu	Phe	Ser	Ser	Asn	Leu	Asp	Pro	Ser	Leu	Val	Glu	Gln	Val	Phe	Leu
						530			535			540			
Asp	Lys	Thr	Leu	Asn	Ala	Ser	Phe	His	Trp	Leu	Gly	Ser	Thr	Tyr	Gln
						545			550			555			560
Leu	Val	Asp	Ile	His	Val	Thr	Glu	Met	Glu	Ser	Ser	Val	Tyr	Gln	Pro
						565			570			575			
Thr	Ser	Ser	Ser	Ser	Thr	Gln	His	Phe	Tyr	Leu	Asn	Phe	Thr	Ile	Thr
						580			585			590			
Asn	Leu	Pro	Tyr	Ser	Gln	Asp	Lys	Ala	Gln	Pro	Gly	Thr	Thr	Asn	Tyr
						595			600			605			
Gln	Arg	Asn	Lys	Arg	Asn	Ile	Glu	Asp	Ala	Leu	Asn	Gln	Leu	Phe	Arg
						610			615			620			
Asn	Ser	Ser	Ile	Lys	Ser	Tyr	Phe	Ser	Asp	Cys	Gln	Val	Ser	Thr	Phe
						625			630			635			640
Arg	Ser	Val	Pro	Asn	Arg	His	His	Thr	Gly	Val	Asp	Ser	Leu	Cys	Asn
						645			650			655			
Phe	Ser	Pro	Leu	Ala	Arg	Arg	Val	Asp	Arg	Val	Ala	Ile	Tyr	Glu	Glu
						660			665			670			
Phe	Leu	Arg	Met	Thr	Arg	Asn	Gly	Thr	Gln	Leu	Gln	Asn	Phe	Thr	Leu
						675			680			685			
Asp	Arg	Ser	Ser	Val	Leu	Val	Asp	Gly	Tyr	Ser	Pro	Asn	Arg	Asn	Glu
						690			695			700			

Pro	Leu	Thr	Gly	Asn	Ser	Ala	Asp	Ile	Gln	His	Ser	Gly	Gly	Arg	Ser
705						710				715					720
Ser	Leu	Glu	Gly	Pro	Arg	Phe	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp
						725				730					735
Leu	Asn	Met	His	Thr	Gly	His									
						740				745					

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<212> PRT
<213> Artificial Sequence

<220>
<223> CA 125/0772P 3-repeat TM

<400>	2														
Ala	Ala	Gln	Pro	Ala	Arg	Arg	Ala	Arg	Arg	Thr	Lys	Leu	Phe	Thr	His
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Arg	Ser	Ser	Val	Ser	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Val	Tyr
									25					30	
Leu	Gly	Ala	Ser	Lys	Thr	Pro	Ala	Ser	Ile	Phe	Gly	Pro	Ser	Ala	Ala
				35				40					45		
Ser	His	Leu	Leu	Ile	Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu
						55				60					
Arg	Tyr	Glu	Glu	Asn	Met	Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
65					70					75				80	
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser
				85				90					95		
Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu
				100				105					110		
Lys	Asp	Gly	Glu	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Pro
				115				120				125			
Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Leu	Glu	Leu
				130			135				140				
Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp
145					150				155				160		
Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Pro
				165				170				175			
Thr	Thr	Ser	Thr	Gly	Val	Val	Ser	Glu	Pro	Phe	Thr	Leu	Asn	Phe	
				180				185				190			
Thr	Ile	Asn	Asn	Leu	Arg	Tyr	Met	Ala	Asp	Met	Gly	Gln	Pro	Gly	Ser
				195				200			205				
Leu	Lys	Phe	Asn	Ile	Thr	Asp	Asn	Val	Met	Lys	His	Leu	Leu	Ser	Pro
				210				215			220				
Leu	Phe	Gln	Arg	Ser	Ser	Leu	Gly	Ala	Arg	Tyr	Thr	Gly	Cys	Arg	Val
225					230				235				240		
Ile	Ala	Leu	Arg	Ser	Val	Lys	Asn	Gly	Ala	Glu	Thr	Arg	Val	Asp	Leu
				245				250			255				
Leu	Cys	Thr	Tyr	Leu	Gln	Pro	Leu	Ser	Gly	Pro	Gly	Leu	Pro	Ile	Lys
				260			265				270				
Gln	Val	Phe	His	Glu	Leu	Ser	Gln	Gln	Thr	His	Gly	Ile	Thr	Arg	Leu
				275			280			285					
Gly	Pro	Tyr	Ser	Leu	Asp	Lys	Asp	Ser	Leu	Tyr	Leu	Asn	Gly	Tyr	Asn
290					295					300					
Glu	Pro	Gly	Pro	Asp	Glu	Pro	Pro	Thr	Thr	Pro	Lys	Pro	Ala	Thr	Thr
305					310				315				320		
Phe	Leu	Pro	Pro	Leu	Ser	Glu	Ala	Thr	Thr	Ala	Met	Gly	Tyr	His	Leu
				325				330			335				
Lys	Thr	Leu	Thr	Leu	Asn	Phe	Thr	Ile	Ser	Asn	Leu	Gln	Tyr	Ser	Pro

340	345	350
Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu		
355	360	365
Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe		
370	375	380
Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala		
385	390	395
Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly		
405	410	415
Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr		
420	425	430
His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu		
435	440	445
Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr		
450	455	460
Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro		
465	470	475
Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val		
485	490	495
Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys		
500	505	510
Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala		
515	520	525
Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu		
530	535	540
Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln		
545	550	555
Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro		
565	570	575
Thr Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr		
580	585	590
Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr		
595	600	605
Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg		
610	615	620
Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe		
625	630	635
Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn		
645	650	655
Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu		
660	665	670
Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu		
675	680	685
Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu		
690	695	700
Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu Ile		
705	710	715
Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val		
725	730	735
Leu Val Thr Thr Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln		
740	745	750
Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu		
755	760	765
Gln Asn Ser Ala Asp Ile Gln His Ser Gly Gly Arg Ser Ser Leu Glu		
770	775	780
Gly Pro Arg Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met		
785	790	795
His Thr Gly His His His His His		
805		800

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<213> Artificial Sequence

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<223> 117.1 VH1 CDR

<400> 3
Gly Phe Ser Leu Ser Thr Pro Gly Met Gly Val Gly
1 5 10

<210> 4
<211> 16
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<213> Artificial Sequence

<220>
<223> 117.1 VH2 CDR

<400> 4
His Ile Trp Trp Asp Asp Phe Lys Arg Asp Asn Pro Ala Leu Lys Ser
1 5 10 15

<210> 5
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 VH3 CDR

<400> 5
Val Asp Gly Asn Phe Leu Ser Trp Tyr Phe Asp Val
1 5 10

<210> 6
<211> 16
<212> PRT
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<220>
<223> 117.1 VL1 CDR

<400> 6
Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 VL2 CDR

<400> 7
Lys Val Ser Asn Arg Phe Ser

1

5

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 VL3 CDR

<400> 8
Ser Gln Ser Arg Tyr Val Pro Glu Thr
1 5

<210> 9
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 368.1 VH1 CDR

<400> 9
Gly Tyr Ser Phe Thr Gly Phe Tyr Met His
1 5 10

<210> 10
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 368.1 VH2 CDR

<400> 10
Tyr Val Ser Cys Tyr Thr Gly Ala Thr Thr Tyr Thr Gln Lys Phe Lys
1 5 10 15
Gly

<210> 11
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 368.1 VH3 CDR

<400> 11
Glu Gly Asp Tyr Tyr Ser Met Asp Phe
1 5

<210> 12
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> 368.1 VL1 CDR

<400> 12
Arg Ser Ser Gln Ser Leu Glu Arg Thr Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> 368.1 VL2 CDR

<400> 13
Lys Val Ser Ser Arg Phe Ser
1 5

<210> 14
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> 368.1 VL3 CDR

<400> 14
Ser Gln Thr Thr His Gly Pro Pro Thr
1 5

<210> 15
<211> 10
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<220>

<223> 501.1 VH1 CDR

<400> 15
Gly Tyr Ile Phe Thr Asp Tyr Gly Met Asn
1 5 10

<210> 16
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> 501.1 VH2 CDR

<400> 16
Cys Ile Asn Thr Tyr Thr Gly Glu Thr Ile Tyr Ser Asp Asp Phe Arg
1 5 10 15
Gly

<210> 17
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<212> PRT
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<223> 501.1 VH3 CDR

<400> 17
Gly Asn Tyr Arg Asp Ala Ile Asp Tyr
1 5

<210> 18
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<212> PRT
<213> Artificial Sequence

<220>
<223> 501.1 VL1 CDR

<400> 18
Lys Ala Ser Gln Asp Ile Lys Ser Tyr Leu Ser
1 5 10

<210> 19
<211> 7
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<220>
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<400> 19
Tyr Ala Thr Thr Leu Ala Asp
1 5

<210> 20
<211> 9
<212> PRT
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<220>
<223> 501.1 VL3 CDR

<400> 20
Leu His His Asp Glu Ser Pro Phe Thr
1 5

<210> 21
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> 776.1 VH1 CDR

<400> 21
Gly Tyr Thr Phe Thr Asp Tyr Asn Ile His
1 5 10

<210> 22
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 VH2 CDR

<400> 22
Tyr Ile Tyr Pro Tyr Asn Gly Val Ser Asp Tyr Asn Gln Asn Phe
1 5 10 15

<210> 23
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 VH3 CDR

<400> 23
Arg Trp Asp Phe Gly Ser Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 24
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 VL1 CDR

<400> 24
Arg Ala Ser Ser Ser Val Ile Tyr Met Cys
1 5 10

<210> 25
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 VL2 CDR

<400> 25
Gly Thr Ser Thr Leu Ala Ser
1 5

<210> 26
<211> 9

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<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 VL3 CDR

<400> 26
Gln Gln Trp Ser Ser Asn Pro Phe Thr
 1           5

<210> 27
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 light chain polypeptide variable region (117.1L)

<400> 27
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
 1           5           10           15
Ser Ser Ser Asp Ala Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 20          25           30
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 35          40           45
Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 50          55           60
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 65          70           75           80
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr
 85          90           95
Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
100         105          110
Ser Gln Ser Arg Tyr Val Pro Trp Thr Phe Gly Gly Thr Lys Leu
115         120          125
Glu Ile Lys
130

<210> 28
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 heavy chain polypeptide variable region (117.1H)

<400> 28
Met Gly Arg Leu Thr Ser Ser Phe Leu Leu Ile Val Pro Ala Tyr
 1           5           10           15
Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 20          25           30
Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 35          40           45
Ser Thr Pro Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
 50          55           60
Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Phe Lys Arg Asp
 65          70           75           80
Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser

```

85

90

95

Ser Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala
100 105 110
Thr Tyr Tyr Cys Val Arg Val Asp Gly Asn Phe Leu Ser Trp Tyr Phe
115 120 125
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135 140

<210> 29

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> 368.1 light chain polypeptide variable region (368.1L)

<400> 29

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15
Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
20 25 30
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
35 40 45
Glu Arg Thr Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
50 55 60
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Ser Arg Phe Ser
65 70 75 80
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr

85 90 95
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe Cys
100 105 110
Ser Gln Thr Thr His Gly Pro Pro Thr Cys Gly Gly Thr Lys Leu
115 120 125
Glu Ile Lys
130

<210> 30

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> 368.1 heavy chain polypeptide variable region (368.1H)

<400> 30

Met Gly Trp Ile Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg
20 25 30
Thr Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
35 40 45
Thr Gly Phe Tyr Met His Trp Val Lys Gln Ser Leu Gly Lys Ser Leu
50 55 60
Glu Trp Ile Gly Tyr Val Ser Cys Tyr Thr Gly Ala Thr Thr Tyr Thr
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Phe Thr Val Asp Thr Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Glu Gly Asp Tyr Tyr Ser Met Asp Phe Trp Gly
115 120 125
Gln Gly Thr Ser Val Thr Val Ser Ser
130 135

<210> 31
<211> 128
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<213> Artificial Sequence

<220>
<223> 501.1 light chain polypeptide variable region (501.1L)

<400> 31
Met Asp Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp
1 5 10 15
Phe Pro Gly Ile Arg Cys Asp Ile Lys Met Thr Gln Ser Pro Ser Ser
20 25 30
Ile Tyr Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser
35 40 45
Gln Asp Ile Lys Ser Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys
50 55 60
Ser Pro Lys Thr Leu Ile Tyr Tyr Ala Thr Thr Leu Ala Asp Gly Val
65 70 75 80
Pro Ser Arg Phe Ser Gly Ser Gly Gln Asp Tyr Ser Leu Ile
85 90 95
Ile Asn Ser Leu Glu Ser Asp Asp Ile Ala Thr Tyr Phe Cys Leu His
100 105 110
His Asp Glu Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125

<210> 32
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<212> PRT
<213> Artificial Sequence

<220>
<223> 501.1 heavy chain polypeptide variable region (501.1H)

<400> 32
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
20 25 30
Pro Gly Glu Thr Val Gln Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe
35 40 45
Thr Asp Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
50 55 60
Lys Trp Met Gly Cys Ile Asn Thr Tyr Thr Gly Glu Thr Ile Tyr Ser
65 70 75 80
Asp Asp Phe Arg Gly Arg Phe Ala Ile Ser Leu Glu Thr Ser Ala Ser
85 90 95

Thr Ala Phe Ile Gln Ile Asn Asn Leu Lys Asn Glu Asp Ala Ala Thr
100 105 110

Tyr Phe Cys Ala Arg Gly Asn Tyr Arg Asp Ala Ile Asp Tyr Trp Gly
115 120 125
Gln Gly Thr Ser Val Thr Val Ser Ser
130 135

<210> 33
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 light chain polypeptide variable region (776.1L)

<400> 33
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Phe Ala Ser Pro Gly Glu Thr Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ile Tyr Met Cys Trp Asn Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Gly Thr Ser Thr Leu Ala Ser Gly Val Pro
65 70 75 80
Thr Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125

<210> 34
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 heavy chain polypeptide variable region (776.1H)

<400> 34
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser His Gly Lys Ile Leu
50 55 60
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Val Ser Asp Tyr Asn
65 70 75 80
Gln Asn Phe Lys Ser Lys Ala Thr Leu Ile Val Asp Asn Ser Ser Asn
85 90 95
Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Trp Asp Phe Gly Ser Gly Tyr Tyr Phe Asp Tyr
115 120 125
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
130 135

<210> 35

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> 117.1 light chain polypeptide variable region (117.1L)

<400> 35

atgaagttgc ctgttaggct gttggtgctg atgttctgga ttccctgggttc cagcagtgtat 60
gctgtgtatga cccaaactcc actctccctg cctgtcagtc ttggagatca ggcctccatc 120
tcttgcagat cttagtcagag ccttgtacac agtaatggaa acacctattt acatttggtac 180
ctgcagaagc caggccagtc tccaaaactc ctgatctaca aagtttccaa ccgattttct 240
ggggtcccag acaggtttagt tggcagttgga tcagggacag atttcacact caggatcagc 300
agagtgaggagg ctgaggatct gggagtttat ttctgtctc aaagtagata tggtccgtgg 360
acgttcgggtg gaggcaccaa gctggaaatc aaa 393

<210> 36

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> 117.1 heavy chain polypeptide variable region (117.1H)

<400> 36

atgggcaggc ttacttcttc attcctgcta ctgattgtcc ctgcataatgt cctgtcccag 60
gttactctga aagagtctgg ccctggata ttgcagccct cccagaccct cagtctgact 120
tgttctttct ctgggttttc actgagcact cctggatgg gtgttaggctg gattcgtcag 180
ccatcagggaa agggtctgga gtggctggca cacatttgggt gggatgattt caagcgccat 240
aatccagccc ttaagagccg actgactatc tctaaggata cctccagcag ccaggtttc 300
ctcaaaatcg ccagtgtgga cactgcagat actgccacat attactgtgt tcgagtggat 360
ggtaacttcc ttcctctggta ttcgatgtc tggggcgctg ggaccacggt caccgtctcc 420
tca 423

<210> 37

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> 368.1 light chain polypeptide variable region (368.1L)

<400> 37

atgaagttgc ctgttaggct gttggtgctg atgttctgga ttccctgtttc cagcagtgtat 60
gctgtgtatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccatc 120
tcttgcagat cttagtcagag ccttgtacac agtaatggaa acacctattt acatttggtac 180
ctgcagaagc caggccagtc tccaaaactc ctgatctaca aagtttccag ccgattttct 240
ggggtcccag ataggtttagt tggcagttgga tcagggacag atttcacact caagatcagt 300
agagtgaggagg ctgaggatct gggaaatttat ttctgtttctc aaactacaca tggtccctccg 360
acgtgcgggtg gaggcaccaa gctggaaatc aaa 393

<210> 38

<211> 411

<212> DNA

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<213> Artificial Sequence

<220>
<223> 368.1 heavy chain polypeptide variable region (368.1H)

<400> 38
atgggatgga tctggatctt tctcttcctc ctgtcaggaa ctgcaggtgt ccactctgag 60
gtccagctgc agcagtctgg acctgagttt gtgaggactg gggcttcagt gaagatatcc 120
tgcaaggcctt ctggttactc attcacttgtt ttctacatgc actgggtcaa gcagagcctt 180
gaaaagagcc ttgagttggat tggatatgtt agttgttaca ctgggtctac tacctacacc 240
cagaagttca agggcaaggc cacatttact gttgacacat cctccagcac agcctacatg 300
caactcaaca gcctgacatc tgaagactct gccgtctattt actgtgcaag agaaggggat 360
tactattcta tggacttctg gggtaagga acctcagtca ccgtctcctc a 411

<210> 39
<211> 386
<212> DNA
<213> Artificial Sequence

<220>
<223> 501.1 light chain polypeptide variable region (501.1L)

<400> 39
atggacatga gggccctgc tcagttttt gggatcttggat tgctctgggtt tccaggtatc 60
agatgtgaca tcaagatgac ccagtctcca tcgtccattt atgcacatcgct gggagagagg 120
gtcaactataa cttgcaaggc gagtcaggac attaaaagctt attaaagctg gtaccaacag 180
aaaccctgaa aatctcctaa gaccctgatc tattatgcaaa caaccctggc agatggggtc 240
ccatcaagat tcagtggcag tggatctggg caagattttt ctctaattcat caacagcctg 300
gagtctgacg atatacgatc ttatttctgtt ctacaccatg atgagagccc attcacgttc 360
ggctcgggaa caaaatttggaa aataaaa 386

<210> 40
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> 501.1 heavy chain polypeptide variable region (501.1H)

<400> 40
atggcttggg tgtggacctt gctgttccctg atggcagctg cccaaagtgc ccaagcacag 60
atccagttgg tgcagtctgg acctgagctg aagaagcctg gagagacagt ccagatctcc 120
tgcaaggcctt ctggctatataa cttcacagac tatggaatga actgggtgaa acaggctcca 180
gaaaagggtt taaaatggat gggctgtata aacacctaca ctggagagac aatataatgt 240
gtgacttca ggggacgggtt tgccatctctt ttggaaacctt ctgccagcac tgcctttatt 300
cagatcaaca acctcaaaaaa tgaggacgcg gcaacatatt tctgtgcaag gggaaattac 360
aggatgctta ttgactattt gggtaagga acctcagtca ccgtctcctc a 411

<210> 41
<211> 383
<212> DNA
<213> Artificial Sequence

<220>
<223> 776.1 light chain polypeptide variable region (776.1L)

<400> 41
atggattttc aagtgcagat tttcagcttc ctgctaattca gtgcttcagt cataatgtcc 60
agaggacaaa ttgttctctc ccagtctcca gcaatcctgtt tgcatctcc aggggagacg 120
gtcacaatga cttgcaggc cagttcaagt gtaatttaca tttgttggaa tcagcagaag 180

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ccaggatcct cccccaaacc ctggatttat ggcacatcca ccctggcttc tggagtcct 240
actcgcttca gtggcagtgg gtctgggacc tc ttactctc tcacaatcag cagagtagag 300
gctgaagatg ctgccactta ttactgccag cagtggagta gtaaccatt cacgttcggc 360
tcggggacaa agttggaaat aaa                                         383

<210> 42
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> 776.1 heavy chain polypeptide variable region (776.1H)

<400> 42
atgggatgga gctggatctt tctttcctc ctgtcaggaa ctgcaggcgt ccactctgag 60
gtccagcttc agcagtcagg acctgagctg gtgaaacctg gggcctcagt gaagatatcc 120
tgcaaggctt ctggatacac attcaactgac tacaacattc actgggtgaa acagagccat 180
ggaaagatcc ttgagtggat tggatattatt tattttata atgggtttc tgactacaac 240
cagaatttca agagaaggc cacattgatt gttagacaatt cctccaacac agcctacatg 300
gaactccgca gcctgacatc tgaggactct gcagtcttattt attgtgcaag atgggacttc 360
ggtagtggct actactttga ctactgggc caaggcacca ctctcacagt ctcctca      417

<210> 43
<211> 45
<212> RNA
<213> Artificial Sequence

<220>
<223> primer (see section 6.6)

<400> 43
rcgacuggag cacgaggaca cugacaugga cugaaggagu agaaa                         45

<210> 44
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> primer (see section 6.6)

<400> 44
gctgtcaacg atacgctacg taacggcatg acagtgtttt tttttttttt tttt                         54

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer (see section 6.6)

<400> 45
ayctcccacac acaggrrcca gtggatagac                                         30

<210> 46
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>		
<223> primer (see section 6.6)		
<400> 46		
ggatacagtt ggtgcagcat c		21
<210> 47		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer (see section 6.6)		
<400> 47		
cgactggagc acgaggacac tga		23
<210> 48		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer (see section 6.6)		
<400> 48		
attaaccctc actaaaggga		20
<210> 49		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer (see section 6.6)		
<400> 49		
taatacgact cactataggg		20
<210> 50		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer (see section 6.6)		
<400> 50		
attaaccctc actaaaggga		20
<210> 51		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer (see section 6.6)		
<400> 51		
taatacgact cactataggg		20

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<210> 52
<211> 383
<212> DNA
<213> Artificial Sequence

<220>
<223> 725.1 light chain polypeptide variable region (725.1L)

<400> 52
atggatttc aagtgcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc 60
agaggacaaa ttattcttc ccagtctcca gcaatcctgt ctgcataatcc agggggagaag 120
gtcacaatga cttgcagggc cagttcaagt gtaagttcca ttcactggta ccagcagaag 180
ccagaatctt cccccaaacc ctggatttac gccacatcca acctggcttc tggagtcct 240
gttcgcttca gtggcagttgg gtctgggacc tcttataactc tcacaatccag cagaatggag 300
gctgcagatg ctgccactta ttactgcccag cagtggagta ttgatccagc cacgttcgga 360
ggggggacca agctggaaat aaa 383

<210> 53
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> 725.1 heavy chain polypeptide variable region (725.1H)

<400> 53
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
 1           5          10          15
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20          25          30
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
 35          40          45
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
 50          55          60
Lys Trp Met Gly Trp Ile Asn Ala Tyr Ile Gly Glu Pro Thr Tyr Ala
 65          70          75          80
Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Ala Ser Thr His
 85          90          95
Thr Ala Tyr Leu Gln Ile Asn Ser Leu Lys Ser Glu Asp Thr Ala Thr
100         105         110
Tyr Phe Cys Ala Ser Gly Gly Asn Ser Leu Asp Phe Trp Gly Gln Gly
115         120         125
Thr Thr Leu Thr Val Ser Ser
130         135

<210> 54
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> 725.1 light chain polypeptide variable region (725.1L)

<400> 54
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1           5          10          15
Val Ile Met Ser Arg Gly Gln Ile Ile Leu Ser Gln Ser Pro Ala Ile
 20          25          30

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Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
35						40						45			
Ser	Ser	Val	Ser	Ser	Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Ser	Ser
50						55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65						70				75			80		
Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Thr	Leu	Thr	Ile
	85					90							95		
Ser	Arg	Met	Glu	Ala	Ala	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
	100					105						110			
Ser	Ile	Asp	Pro	Ala	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	
	115					120						125			

<210> 55
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> 16H9 heavy chain polypeptide variable region (16H9H)

<400>	55														
Met	Lys	Cys	Ser	Trp	Val	Ile	Phe	Phe	Leu	Met	Ala	Val	Val	Thr	Gly
1					5				10					15	
Val	Asn	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys
					20				25					30	
Pro	Gly	Ala	Ser	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile
					35			40				45			
Lys	Asp	Thr	Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu
					50			55			60				
Glu	Trp	Ile	Gly	Arg	Ile	Asp	Pro	Ala	Asn	Gly	Asn	Thr	Lys	Tyr	Asp
					65			70			75			80	
Pro	Lys	Phe	Gln	Gly	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn
					85			90					95		
Thr	Ala	Tyr	Val	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val
					100			105				110			
Tyr	Tyr	Cys	Ala	Ser	Ser	Asp	Ile	Tyr	Tyr	Gly	Asn	Pro	Gly	Gly	Phe
					115			120			125				
Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala			
					130			135			140				

<210> 56
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> 16H9 light chain polypeptide variable region (16H9L)

<400>	56														
Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1						5			10			15			
Val	Ile	Met	Ser	Arg	Gly	Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile
						20			25			30			
Met	Ser	Ala	Ser	Leu	Gly	Glu	Arg	Val	Thr	Met	Thr	Cys	Thr	Ala	Ser
						35			40			45			
Ser	Ser	Val	Ser	Ser	Ser	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly
						50			55			60			

Ser Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
65 70 75 80
Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
85 90 95
Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His
100 105 110
Gln Tyr His Arg Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
115 120 125
Ile

<210> 57

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> 725.1 heavy chain polypeptide variable region (725.1H)

<400> 57

atggcttggg tgtggacatt gctattcctg atggcagctg cccaaagtgc ccaagcacag 60
atccagttgg tgcatgtctgg acctgaactg aagaaggctg gagagacagt caagatctcc 120
tgcaaggctt ctggatattc cttcacaaac tatggaatga actgggtgaa gcaggctcca 180
gggaagggtt taaagtggat gggctggata aacgcctaca ttggagagcc aacatatgct 240
gatgacttca agggacgatt tgccttcctt ctggaaagcct ctaccacac tgcctatttg 300
cagatcaaca gcctcaaaaag tgaggacacg gctacatatt tctgtcaag tgggggtaac 360
tcccttgact tttggggcca aggcaccact ctcacagtct cctcag 406

<210> 58

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> 16H9 heavy chain polypeptide variable region (16H9H)

<400> 58

atgaaatgca gctgggttat cttcttcctg atggcagtgg ttacaggggt caattcagag 60
gttcagctgc agcagtctgg ggcagagctt gtgaagccag gggcctcagt caagttgtcc 120
tgcacagctt ctggcttcaa cattaaagac acctatatgc actgggtgaa gcagaggcct 180
gaacagggcc tggagtggat tggaaaggatt gatcctgcga atggtaatac taaatatgac 240
ccgaagttcc agggcaaggc cactataaca gcagacacat cctccaacac agcctacgtg 300
cagctcagca gcctgacatc tgaggacact gccgtctatt actgtgcttag tagtgacatc 360
tactatggta accccggggg gtttgcttac tggggccaag ggactctggt cactgtctct 420
gca 423

<210> 59

<211> 389

<212> DNA

<213> Artificial Sequence

<220>

<223> 16H9 light chain polypeptide variable region (16H9L)

<400> 59

atggattttc aggtgcagat tttcagcttc ctgctaattca gtgcctcagt cataatgtcc 60
agaggacaaa ttgttctcac ccagtctcca gcaatcatgt ctgcacatcttctt aggggaacagg 120
gtcaccatga cctgcactgc cagctcaagt gtaagttcca gttacttgca ctggtaccag 180
cagaagccag gatccccc caaactctgg atttatagca catccaacct ggcttctgga 240
gtcccagctc gttcagtg gttgggtctt gggaccttctt actctctcac aatcagcagc 300

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atggaggctg aagatgctgc cacttattac tgccaccagt atcatcggttc cccattcacy 360
ttcggctcg ggacaaagtt ggaaataaa 389

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 725.1 VH1 CDR

<400> 60
Gly Tyr Ser Phe Thr Asn Tyr Gly Met Asn
1 5 10

<210> 61
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 725.1 VH2 CDR

<400> 61
Trp Ile Asn Ala Tyr Ile Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
1 5 10 15
Gly

<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 725.1 VH3 CDR

<400> 62
Gly Gly Asn Ser Leu Asp Phe
1 5

<210> 63
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 725.1 VL1 CDR

<400> 63
Arg Ala Ser Ser Ser Val Ser Ser Ile His
1 5 10

<210> 64
<211> 7
<212> PRT
<213> Artificial Sequence

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<220>

<223> 725.1 VL2 CDR

<400> 64

Ala Thr Ser Asn Leu Ala Ser
1 5

<210> 65

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 725.1 VL3 CDR

<400> 65

Gln Gln Trp Ser Ile Asp Pro Ala Thr
1 5

<210> 66

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 16H9 VH1 CDR

<400> 66

Gly Phe Asn Ile Lys Asp Thr Tyr Met His
1 5 10

<210> 67

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 16H9 VH2 CDR

<400> 67

Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe Gln
1 5 10 15
Gly

<210> 68

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 16H9 VH3 CDR

<400> 68

Ser Asp Ile Tyr Tyr Gly Asn Pro Gly Gly Phe Ala Tyr

1

5

10

<210> 69
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 16H9 VL1 CDR

<400> 69
Thr Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His
1 5 10

<210> 70
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 16H9 VL2 CDR

<400> 70
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 71
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 16H9 VL3 CDR

<400> 71
His Gln Tyr His Arg Ser Pro Phe Thr

1

5